

# REPLACEMENT SHEET

1/13

The intron sequences between exons 2 - 3 and exons 18 - 19 are missing (introns: small letters, exons: capital letters). Small letters in the first exon indicate nucleotides that have not been unambiguously determined.

*Exon 1*

```

1  CGGGTGAATC CCGGCGCCGC GCCCGGACC CGCAGCTCCC TGCACCTCTC
51  CCTCCCAGCC GCTTTAACAC CCACACCCCA CAGTCTCTCC CACGsCCGCG
101 CCTTGGCGGC CCCACTGAAT CCCTACGCGG GGCCAGCGG TACCGGGAGA
151 CCGGGCTAGC CTATGGGAGC GCCCAGATAA CGCGGGTTGG GGGCGCCCGC
201 GCCCCcATCC CCGCCAGCAT GACTCGATCG CCGCCCCCTCA GAGAGCTGCC
251 CCCGAGTTAC ACACCCCCAG CTCGAACCGC AGCACCCCAG gtgagtagag
301 ggggagctgg aagaaggaag agagcggagc caggtctgtc actcgggcct
351 ctgcaagggt tgtgatgtct tgaagtgccg agtgtcatta gatgtctgaa
401 ggcaagttag agccagcacc gcaagcaagt tgtgcgtgtg tgcggtgtg
451 tctgtgccgg tgtctcctca tcgtctggcc agtgagaatg aatgtctgtg
501 ggttcacctc tgtgtccacc cgacgacagg tgtgtgtaca tatgtatcct
551 gctctcagaa aatgggccta tgccgccggg cgcggtgact cacgcctgta
601 atcccaacac tgggaggctg aggcaggcag attacctgag gtcaggaggt
651 cgagaccagc caggccaaca tggggaaact ctgtctctac taaaaataaa
701 aattagcagg gcgtggtggc gggcgccctgt agtcccaact actcgggagg
751 ctgaggcagg agaatctctt gaacctggga ggcggagggt gcagtcaagc
801 cgagatcaca cactgcact ccagccaggg caacagagcg agatgcgtct
851 caaaaaaaaa aaaaaaaaaa aaaaggagag aaaacaaaaa gaaaagaaag
901 gaaaataggc ctatgccttc ctcagggtgtg tgctggggat ggtgggtggt
951 acatcttcca agtctgggcc tgtgtctgtg ttggtgctcc ctgtcccaca
1001 tccagaaatc aagaagcgag ggctgggcag cagatatata gggtgagaag
  
```

Fig.1A

# REPLACEMENT SHEET

2/13

```

1051 ggaaggattt catgcattgt tacagtgatg cctggctgac ctttctcttt
      EXON 2
1101 ccatcccagA TCCTAGCTGG GAGCCTGAAG GCTCCACTCT GGCTTCGTGC
1151 TTA CTTCAG GGCCTGCTCT TCTCTCTGGG ATGCGGGATC CAGAGACATT
1201 GTGGCAAAGT GCTCTTTCTG GGACTGTTGG CCTTTGGGGC CCTGGCATT A
1251 GGTCTCCGCA TGGCCATTAT TGAGACAAAC TTGGAACAGC TCTGGGTAGA
1301 AGTGGGCAGC CGGGTGAGCC AGGAGCTGCA TTACACCAAG GAGAAGCTGG
1351 GGGAGGAGGC TGCATACACC TCTCAGATGC TGATACAGAC CGCACGCCAG
1401 GAGGGAGAGA ACATCCTCAC ACCCGAAGCA CTTGGCCTCC ACCTCCAGGC
1451 AGCCCTCACT GCCAGTAAAG TCCAAGTATC ACTCTATGGG AAG.....
1501 .....g
1551 tgagtctggc tgagccctg agcagctggg ggcgaggcgt gctgtggggg
1601 ttctggagtg ggaatccctt tcttctgctg atctcctatg cccctggcta
      EXON 4
1651 ttgcagTCCT GGGATTTGAA CAAAATCTGC TACAAGTCAG GAGTTCCCCCT
1701 TATTGAAAAT GGAATGATTG AGCGGgtaag tgtcctgaga gggagtagag
1751 gcagaacttt ttctgtagcg tgggaggact cagagaccga gcaagcccca
1801 cagcctgcaa tctgccccct taaaactaag gagggggatt gcagagggga
1851 tcctacaaag gttgtggggc aggactgacg tggcccgggg tatccctggc
      EXON 5
1901 agATGATTGA GAAGCTGTTT CCGTGCGTGA TCCTCACCCC CCTCGACTGC
1951 TTCTGGGAGG GAGCCAAACT CCAAGGGGGC TCCGCCTACC TGCCgtgagt
2001 gccactcctg gggccctgct tcatctcccg ctggggactc tcccagcaga
2051 aaggaggggt ctggggaatg aggatgatca aaaccttacc aaggtcctaa
2101 ttacctcca ggccaggaac agagagcatg ggcttcccca aggtctctctc
2151 cacatcctcc ttctctttcc ctctcaagga aggaagacct gacttattta
2201 cacaaaacta aacacaaaga tctgtaagat ctgagcaaag gagaaaaaga
2251 tccccacaaa gaggccttgc tgggggaaat tacctaggtg tttgctaagc
2301 cattgcccag gccagaaaga aaacctgcta caggcatgtg cctgctggtt
2351 gtatattaga accaagcaca cagcttggtg aggaactcag tggggccttt

```

Fig.1B

# REPLACEMENT SHEET

3/13

2401 ctgggcccctt tctatgtatt aggtaaccct gccctgatat tcgtctcagc  
 2451 cccttggtact cttctacagc tctactgtage accctgggtg gcccatgcag  
 2501 cctggcagtt ctgagaagct gaggcttgca caccctccat atggaaggac  
 2551 aaatcggcag ataagaggag ggtgggggtac agcatggcgc cccagcagca  
 2601 gtttggagcc tgggttttcg tccctgacct tcaccaacta taggcttttc  
 2651 cctcagCGGC *EXON 6* CGCCCGGATA TCCAGTGGAC CAACCTGGAT CCAGAGCAGC  
 2701 TGCTGGAGGA GCTGGGTCCC TTTGCCTCCC TTGAGGGCTT CCGGGAGCTG  
 2751 CTAGACAAGG CACAGGTGGG CCAGGCCTAC GTGGGGCGGC CCTGTCTGCA  
 2801 CCCTGATGAC CTCCACTGCC CACCTAGTGC CCCCACCAT CACAGCAGGC  
 2851 AGgtgggttc caaccaggtc tgccaggga aggtgtttt cttcccttt  
 2901 cccttcctca tactcctgtg ttctggggga gctgactgct ctgtgccttg  
 2951 accccccact tcctggccat tattaccctg ctcccacagt gccaggcccc  
 3001 caatgttcca ttccattca gttatcctac ggagccctca agtggatat  
 3051 atgaatccct ttttccttt ctaagcctag ataaggctgg acttcttttt  
 3101 tttttttttt ttgagtctca ctctgtcacc caggctggag tgcagtagtt  
 3151 cgatcttggc tctctgcaac ctctggtcaa gcaattctcc tgccttagcc  
 3201 tcctgagtag ctgggattac aggtgcccac caccatgccc ggctaatttt  
 3251 tattagcctc ccaaagtgt gggattacag gcgtgagcca ctgcgcctgg  
 3301 ccaaggctgg actttttatc aaaatagact aatacaggga aactaagaac  
 3351 acagcaggta agcatgaata tcatacctgg tttcccaggt ttctttgtgg  
 3401 ccctgcaa at gtggtacttt tttcagaatc cgccagttac accagtcct  
 3451 cccagaagcc tacttccagg cctctgcttc cccttggggc ttctgtctg  
 3501 cgggatacta gctgttctact cctgcagagc agtcaagagg ctgagaatag  
 3551 ttacctacac tccagcccta ctgagcttca tggcagcgtg gttcctggag  
 3601 gtggaagccc agggacactc agttatccac ggccagggcc ttgagcatta  
 3651 acccctcctg tttccctcca *EXON 7* gGGCTCCCAA TGTGGCTCAC GAGCTGAGTG  
 3701 GGGGCTGCCA TGGCTTCTCC CACAAATTCA TGCCTGGCA GGAGGAATTG

Fig.1C

# REPLACEMENT SHEET

4/13

```

3751 CTGCTGGGAG GCATGGCCAG AGACCCCCAA GGAGAGCTGC TGAGGtaggg
3801 tctcctctgg gagttggtga ggggactctg ttcattgagaa cccatactgt
3851 aatgccaggc agctctggca aaaggccctt cacatccctc accaggtggt
3901 tggggcagct ctgacccttg gttctccac acccccacca gGGCAGAGGC
3951 CCTGCAGAGC ACCTTCTTGC TGATGAGTCC CCGCCAGCTG TACGAGCATT
4001 TCCGGGGTGA CTATCAGACA CATGACATTG GCTGGAGTGA GGAGCAGGCC
4051 AGCACAGTGC TACAAGCCTG GCAGCGGCGC TTTGTGCAGg tcggtatgga
4101 caaggacaag gggggtgccc tgaggccatt cctcctcct gccccctcct
4151 atccaccctg tttctccagC TGGCCAGGA GGCCCTGCCT GAGAACGCTT
4201 CCCAGCAGAT CCATGCCTTC TCCTCCACCA CCCTGGATGA CATCCTGCAT
4251 GCGTTCTCTG AAGTCAGTGC TGCCCGTGTG GTGGGAGGCT ATCTGCTCAT
4301 Ggtgggtctt gcacctggca ccttgcccc accccacctc caaccagtgc
4351 ccaccctggg agcccttgag actgccctt cccccacag CTGGCCTATG
4401 CCTGTGTGAC CATGCTGCGG TGGGACTGCG CCCAGTCCCA GGGTTCCGTG
4451 GGCCTTGCCG GGGTACTGCT GGTGGCCCTG GCGGTGGCCT CAGGCCTTGG
4501 GCTCTGTGCC CTGCTCGGCA TCACCTCAA TGCTGCCACT ACCCAGgtac
4551 gccaggactg cagggcagac tcagtgccag tcaccaggct tcacgggtcc
4601 tcagctgccc gctcctctgc cctccagGT GCTGCCCTTC TTGGCTCTGG
4651 GAATCGGCGT GGATGACGTA TTCCTGCTGG CGCATGCCTT CACAGAGGCT
4701 CTGCCTGGCA CCCCTCTCCA Ggtggggcct tgtccccag ggctcatctg
4751 aggcagctca gcttactggt taagagcctc ttggttcaag tgacccttgg
4801 gctgctaatag aacctcgggtg cctcttgtcc ccatctgtaa acaggggaaa
4851 taatagtgtg gtgtcctaag gggtattggt tggatcagtg aggttaactca
4901 agttgaatgc ttagaacagc ccatcatag tacatggtac ccaataaatg
4951 ctagccactg tggtatgact gccccacctc tgcaccccaa gttcctgagc
5001 ctccccctca ctccactttg acacggcccc tcccttgtga cctgagggca
5051 ggtccccact ctgtcctggc agGAGCGCAT GGGCGAGTGT CTGCAGCGCA

```

Fig.1D

# REPLACEMENT SHEET

5/13

5101 CGGGCACCAG TGTCGTACTC ACATCCATCA ACAACATGGC CGCCTTCCTC  
 5151 ATGGCTGCCC TCGTTCCCAT CCCTGCGCTG CGAGCCTTCT CCCTACAGGC  
 5201 GGCCATAGTG GTTGGCTGCA CCTTTGTAGC CGTGATGCTT GTCTTCCCAG  
 5251 CCATCCTCAG CCTGGACCTA CGGCGGCGCC ACTGCCAGCG CCTTGATGTG  
 5301 CTCTGCTGCT TCTCCAGgta ctgcggtgcgc cccagccccct tcctccccgtg  
 5351 acccagccca gcctgtcccc tcaccagcat ttcaaggcac agacctgtca  
 5401 tccactctct acctcttcca gTCCCTGCTC TGCTCAGGTG ATTCAGATCC  
 EXON 13  
 5451 TGCCCCAGGA GCTGGGGGAC GGGACAGTAC CAGTGGGCAT TGCCCACCTC  
 5501 ACTGCCACAG TTCAAGCCTT TACCCACTGT GAAGCCAGCA GCCAGCATGT  
 5551 GGTCACCATC CTGCCTCCCC AAGCCACCT GGTGCCCCCA CCTTCTGACC  
 5601 CACTGGGCTC TGAGCTCTTC AGCCCTGGAG GGTCCACACG GGACCTTCTA  
 5651 GGCCAGGAGG AGGAGACAAG GCAGAAGGCA GCCTGCAAGT CCCTGCCCTG  
 5701 TGCCCGCTGG AATCTTGCCC ATTTGCGCCG CTATCAGTTT GCCCCGTTCG  
 5751 TGCTCCAGTC ACATGCTAAG gtaagactgg gcagagcagg gcagagactt  
 5801 agcatctctg ggcccagaag ggcagagagg gcttagtcca ctgcctgagg  
 5851 ggctgggggc agccctgggg tctccagctt agttgctaca tcccgcagGC  
 EX  
 XON 14  
 5901 CATCGTGCTG GTGCTCTTTG GTGCTCTTCT GGGCCTGAGC CTCTACGGAG  
 5951 CCACCTTGGT GCAAGACGGC CTGGCCCTGA CGGATGTGGT GCCTCGGGGC  
 6001 ACCAAGGAGC ATGCCTTCCT GAGCGCCCAG CTCAGGTACT TCTCCCTGTA  
 6051 CGAGGTGGCC CTGGTGACCC AGGGTGGCTT TGA CTACGCC CACTCCCAAC  
 6101 GCGCCCTCTT TGATCTGCAC CAGCGCTTCA GTTCCCTCAA GGCGGTGCTG  
 6151 CCCCCACCGG CCACCCAGGC ACCCCGCACC TGGCTGCACT ATTACCGCAA  
 6201 CTGGCTACAG Ggtgagaggc gaggagacgg gcagggaggg gtgctgcagg  
 6251 gagaaacgcc ctggggccac cagctaata g aaccctatcc tgggtctcccc  
 EXON 15  
 6301 cagGAATCCA GGCTGCCTTT GACCAGGACT GGGCTTCTGG GCGCATCACC  
 6351 CGCCACTCGA CCGCAATGGC TCTGAGGATG GGGCCCTGGC CTACAAGCTG  
 6401 CTCATCCAGA CTGGAGACGC CCAGGAGCTT CTGGATTTC GCCAGgttgg

Fig.1E

# REPLACEMENT SHEET

6/13

6451 gagagggctg gaggggtcca ctagtacagg ggctgcaggc ctcctgggcc  
EXON 16  
6501 caggccttca gccctctctg cctctgcagC TGACCACAAG GAAGCTGGTG  
6551 GACAGAGAGG GACTGATTCC ACCCGAGCTC TTCTACATGG GGCTGACCGT  
6601 GTGGGTGAGC AGTGACCCCC TGGGTCTGGC AGCCTCACAG GCCAACTTCT  
6651 ACCCCCCACC TCCTGAATGG CTGCACGACA AATACGACAC CACGGGGGAG  
6701 AACTTTCGCA gtgagtcttg gggggagctc ggcaagagcc tcagcctcgc  
6751 ccacacaagc cctgagcctg aggccctgcc cactctgccc cgtgctcacc  
EXON 17  
6801 gccctgtccc tctccctctt ctcccttccc ctcccttcca cagTCCCGCC  
6851 AGCTCAGCCC TTGGAGTTTG CCCAGTTCCC TTTCTGCTG CGTGGCCTCC  
6901 AGAAGACTGC AGACTTTGTG GAGGCCATCG AGGGGGCCCCG GGCAGCATGC  
6951 GCAGAGGCCG GCCAGGCTGG GGTGCACGCC TACCCCAGCG GCTCCCCCTT  
7001 CCTCTTCTGG GAACAGTATC TGGGCCTGCG GCGCTGCTTC CTGCTGGCCG  
7051 TCTGCATCCT GCTGGTGTGC ACTTTCCTCG TCTGTGCTCT GCTGCTCCTC  
7101 AACCCTTGA CGGCTGGCCT CATAgtagt gcttgcagga gtggggacag  
7151 agacacccca cccttccctg cccagcctgt catccctcct gccaggagcc  
EXON 18  
7201 ctctgtgagc cctgtctccc tcagGTGCTG GTCCTGGCGA TGATGACAGT  
7251 GGAACCTTTT GGTATCATGG GTTTCCTGGG CATCAAGCTG AGTGCCATCC  
7301 CCGTGGTGAT CCTTGTGGCC TCTGTAGGCA TTGGCGTTGA GTTCACAGTC  
7351 CACGTGGCTC TGGGCTTCCT GACCACCCAG GGCAGCCGGA ACCTGCGGGC  
7401 CGCCCATGCC CTTGAGCACA CATTTGCCCC CGTGACCGAT GGGGCCATCT  
7451 CCACATTGCT GGGTCTGCTC ATGCTTGCTG GTTCCCATT TGACTTCATT  
7501 GTAAG.....  
7551 ..... gtagggaggg ctcggggcag ggaggcagg ctcaggacag  
EXON 20  
7601 gcctgggctg actccccca caccctaccc ctagGTACTT CTTTGC GGCG  
7651 CTGACAGTGC TCACGCTCCT GGGCCTCCTC CATGGACTCG TGCTGCTGCC  
7701 TGTGCTGCTG TCCATCCTGG GCCCGCCGCC AGAGgtgacc acaccctcgg  
7751 caccatccct ctactcccag cccaagggac ggggtaggga gaggcaaggg

Fig.1F

# REPLACEMENT SHEET

7/13

7801 aagggacaga gccctgtggc ccacagacag gtacctcccc aacaggtgcc  
 7851 accagctgaa ggtggcagcc tcctcctttc cccagacacc atgttcctgc  
 7901 ccctcagccc tcctggcttc ttcattgggac ccaccttaga ctttttaggat  
 7951 ccagaacaag gtgcagggtt tgccccaggc ctcaacatcc tgtcgccctgc  
 8001 cagctctcat atcctgctgg agaccaacaa gggccccagc ttcccaacag  
 8051 tcatggtaat cccagcgag atgctaaagg ggacgggagc cccagggggc  
 8101 cgtgggctta ctggggctgg tgtctcccca <sup>EXON 21</sup> cagGTGATAC AGATGTACAA  
 8151 GGAAAGCCCA GAGATCCTGA GTCCACCAGC TCCACAGGGA GCGGGGCTTA  
 8201 Ggtggggggc atcctcctcc ctgccccaga gctttgccag agtgactacc  
 8251 tccatgaccg tggccatcca cccaccccc ctgcctggtg cctacatcca  
 8301 tccagcccct gatgagcccc cttggtcccc tgctgtcact agctctggca  
 8351 acctcagttc caggggacca ggtccagcca ctgggtgaaa gagcagctga  
 8401 agcacagaga ccatgtgtgg ggcgtgtggg gtcactggga agcactgggt  
 8451 ctggtgttag acgcaggatg gacccttgga gggctctgct gctgctgcat  
 8501 cccctctccc gaccagctg tcatgggcct ccctgatatc catacagaac  
 8551 agccaccgat ttgcacatcc aggctgtgt gagcctgtat ctgtgtcact  
 8601 tgagagtga agctggcact tggggctgca gtgcagccct gtcctcttc  
 8651 ccacccaca cactgcctg cccagctgac caagcctgag ggacctcca  
 8701 gcaccttcc gtctggtgac tcctgggcag gctctccata tcctgccc  
 8751 cctcctacca catccattat ttatatgaaa atgtctatct tttgagtata  
 8801 catacatgtt agctatgatg aaagttttat tttttaaaga atgaaatata  
 8851 ttctatgtga agctatgatg aaagttttat tttttaaaga atgaaatata  
 8901 ttctatgtga actaatctcg aaagttttat tttttaaaga atgaaatata  
 8951 ttctatgtgt gcaagtgaac attagcttca gttgcttttt tttggacaga  
 9001 gtggggagtt tgcaagtga cattagctat tggaaggagc ttctctggtg  
 9051 ccaggacctg aggtattagc ttctctagtt ctgggtggaa aagacccag  
 9101 attctggatt tttgtcatat acttggtaac atcatctgga ttaagtgtt

Fig.1G

# REPLACEMENT SHEET

8/13

9151 actatacaaa acgataacaa attttgttgg tgtgaaatcc tactgggttc  
 9201 aatctggaga ccgagagcag aaaaaaaga accccactgt gtggctttca  
 9251 gagccaccat attccagcct gcccgctctct ccagactcac ctccacctac  
 9301 ctgcttcacc cgcacgggaa acggcaaggc agaggggcaa agccatgcag  
 9351 caggtggaag gcgaggtgga ggcagatcag gaaagcagcc agttgaagca  
 9401 gagagaggtc aacagggctt ggggagcttc tcaggaggtt tgtggacca  
 9451 gggaaaggag ccaggttcca gagcaacctc caaggcaaag gcctctgtaa  
 9501 gttggttgtc ctgacagccg agaggtgtct ttggccagtc agccagtgga  
 9551 tcagttgctg gaactgctca gaaactgagg tgctagcagt tagtgaggac  
 9601 acagcgtaag ttgtttgttc tgtgaaagtt gaacagctcc actaagcaga  
 9651 ggccttgaag agtggccaca gccctggaat agagcacaga gcctcaccta  
 9701 gaggcgtggg gaggtttgca actgcccctt cccagccata gcttaggacc  
 9751 catagtctag ttcacataga ccctgggctc caaccacca ctcaccagga  
 9801 atgatccac cccaggaaca atgcgttctc acatcccacc ccacctggac  
 9851 aaaggccagg aaatcatggt ctgacaaaaa gatacaacaa caaaaacaac  
 9901 aacaacaaaa aacgcctatt gcaattgaat ccacgctaaa atgcctaaaa  
 9951 agctcaagag aagcgggtag ttggcagaga acctagagta gggggtgcaa  
 10001 ccagcaggcc caagggaggg aggetgcatt tgggtccagc agtgtttggg  
 10051 tcaccaagaa gggccttcta ggtggagcag agagagctca ccaggccaga  
 10101 atagtgcaa gggggtcagc cctcagtgcc acttaccagc ggagtaaccc  
 10151 tgggcaagtt agccagcctc actaagcctc cccatcttca tctttccagG  
 XON 22  
 10201 CCCGAGGAGA TC**TAG**CCTCT GCCTCCCACC CCAGCACCCC CTCATCAGAC  
 10251 ACAAGGAGCG CCACTGTCTG GACAGGCTGA ATTGGTCTTC GGGTCCCTAA  
 10301 TTTCTCATAC GCCATTCCCT CTGCCTAGAA CACTTTCTCA CCTCCCCTTG  
 10351 ATGTGACCCC ATATCACCTT TCGAGGTGAA TTGGATCGGA TGCCATCTCC  
 10401 TCCAGGAGGG GTGGGGTCGT GCCTCCTGTG AGGTCCCAGT GCCCCTGAGT  
 10451 GTCTGTGCCC GTCTGTTTCC CCGTCCCTCT CTCTAAGCCC GGAGGCTTAC

Fig.1H



# REPLACEMENT SHEET

9/13

10501 TGCGGGTAAG GACGGCGGGA CAGGACCTTA ACCCCTGGGA CGAACACCAG  
10551 CTCCGCAAAG GACTCCGCAC CCGGCGCCGC CCACGGGGTG CGGGTCCCAG  
10601 GAGGACCAGC AGAGAGGAGC ATAGGAGAGC AAAGGAGATC AGTGACCCAT  
10651 GGCTTCCCCG GTGGCGCGGA ACAGCCCGGA GCCGCCTGTG ATTTGCATAC  
10701 CCATGGTGCA CCACGAAAAG ATACCCTCAA GATGCTTGCA CTCCCTCTGT  
10751 GCGCGCATTT CTGCACTGTT TTAGAGCATG ATGCCTCTTA CACGCATCTG  
10801 TGTGCATAAA CTACATATAG GGAGTGCGTA CCACGCAGGC ATCCAACAAC  
10851 CATAAGTGTG TTAAGTGTTA GTTCTCCCTG CGAGGTTCGA AGCGGAAGTC  
10901 ACGAATATAC TCGGGTTTCT CTTCAAAGCG CATAAATCTT TCGCCTTTTA  
10951 CTAAAGATTT CCGTGGAGAG AAAGTTGTGA GTTTTATTC AATTTTTTGA  
11001 GGCCTCTTAT TTCCTGAGGC TACATTTTAA AGTATTAAAA GTTAGGCAAC  
11051 TACAAAAAAA AAAAAAAA

Fig.1I

# REPLACEMENT SHEET

10/13

```

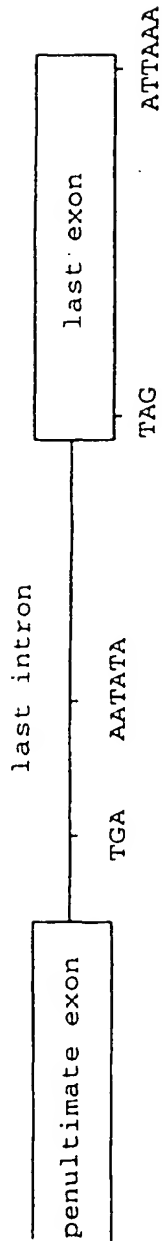
1 .....MTRSPPLRELP..... 11
  |...|
1 MASAGNAAE PQDRGGGSGCIGAPGRPAGGGRRRRTGGLRRAAAPDRDYL 50
12 ..PSYTPPARTAAPQI...LAGSLKAPLWLRAYFQGLLFSLGCGIQRHCG 56
  |||...| |...| |...| |...| |...| |...| |...|
51 HRPSYCDAA.FALEQISKGKATGRKAPLWLRKFQRLLFKLGCIYQKNCG 99
57 KVLFLGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGE 106
  |...| |...| |...| |...| |...| |...| |...| |...|
100 KFLVVGLLIFGAFVGLKAANLETNVEELWVEVGGRVSRELNTRYQKIGE 149
107 EAAYTSQMLIQATARQEGENILTPEALGLHLQAALTASKVQVSLYGKSWDL 156
  ||...| |...| |...| |...| |...| |...| |...| |...|
150 EAMFNPQLMIQTPKEEGANVLTTEALLQHLDLSALQASRVHVYMYNRQWKL 199
157 NKICYKSGVPLIENGMIERMIEKLFPCVILTPLDCFWEAKLQGG SAYLP 206
  :...| |...| |...| |...| |...| |...| |...| |...|
200 EHLCKYSGELITETGYMDQIIEYLYPCLIIITPLDCFWEAKLQSGTAYLL 249
207 GRPDIQWTNLDPEQLLEELGPFA.SLEGFRELLDKAQVGQAYVGRPCLHP 255
  |...| |...| |...| |...| |...| |...| |...| |...|
250 GKPLRLWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGYMDRPNLP 299
256 DDLHCPPSAPNHHSRQAPNVAHELSSGGCHGFSHKFMHWQEELLGGMARD 305
  .|...| |...| |...| |...| |...| |...| |...| |...|
300 ADPDCPATAPNKNSTKPLDMALVLNCGCHGLSRKYMHWQEELIVGGTVKN 349
306 PQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAW 355
  .|...| |...| |...| |...| |...| |...| |...| |...|
350 STGKLVSAAHALQTMFQLMTPKQMYEHFKGYEYVSHINWNEDKAAAILAW 399
356 QRRFVQLAQEALPENASQQIHAFSSTLDDILHAFSEVSAARVVGGYLLM 405
  ||...| |...| |...| |...| |...| |...| |...| |...|
400 QRTYVEVVHQSV AQNSTQKVLSTTTTLLDDILKSFSDVSVIRVASGYLLM 449
406 LAYACVTMLRWDCAQSGSVGLAGVLLVALAVASGLGLCALLGITFNAAT 455
  ||...| |...| |...| |...| |...| |...| |...| |...|
450 LAYACVTMLRWDCSKSQGAVGLAGVLLVALSVAAGLGLCSLIGISFNAAT 499
456 TQVLPFLALGIGVDDVFLLAHAFTEALPG..TPLQERMGECLQRTGTSVV 503
  ||...| |...| |...| |...| |...| |...| |...| |...|
500 TQVLPFLALGVGVDDVFLLAHAFSETGQNKRIPFEDRTGECLKRTGASVA 549
504 LTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVMLVFPAIISLD 553
  ||...| |...| |...| |...| |...| |...| |...| |...|
550 LTSISNVTAFFMAALIPIPALRAFSLQAAVVVVFNFAMVLLIFPAIISMD 599
554 LRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGT.....VPVG 592
  |...| |...| |...| |...| |...| |...| |...| |...|
600 LYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPYSSHS 649
593 IAH.....LTATVQAFTHCEASSQHVVITLPPQAH.....VPPPSDPLGS 633
  :||...| |...| |...| |...| |...| |...| |...| |...|
650 FAHETQITMQSTVQLRTEYDPHTHVYTTAEPRSEISVQPVTVTQDTLSC 699

```

Fig.2A

11/13

## Genomic



GlyLeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThr  
 GGCCTTAGgtgggggcatcctcctccctgccccagagctttgccagagtgact  
 -----C-----acaggc--c--a-----t-----

ThrSerMetThrValAlaIleHisProProProLeuProGlyAlaTyIleHis  
 acctccatgaccgtggccatccaccacccccctgcctggcctacatccat  
 -----t-----C-----a--t-----a--a--g---c

ProAlaProAspGluProProTrpSerProAlaAlaThrSerSerGlyGlnLeu  
 ccagccctgatgagcccccttggtccctgctgcccactagctctggcaacctc  
 -----t-c--g-----a-a-a-\*

SerSerArgGlyProGlyProAlaThrGly \* gProAsnAsnIle \*  
 agttccaggggaccaggtccagccactgggtga.....agCCCCGAGGAGATCTAG

Parotid gland  
Colon

## Fetal brain

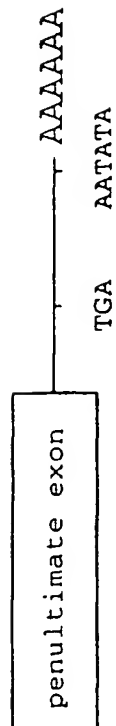


Fig.2B

# REPLACEMENT SHEET

12/13

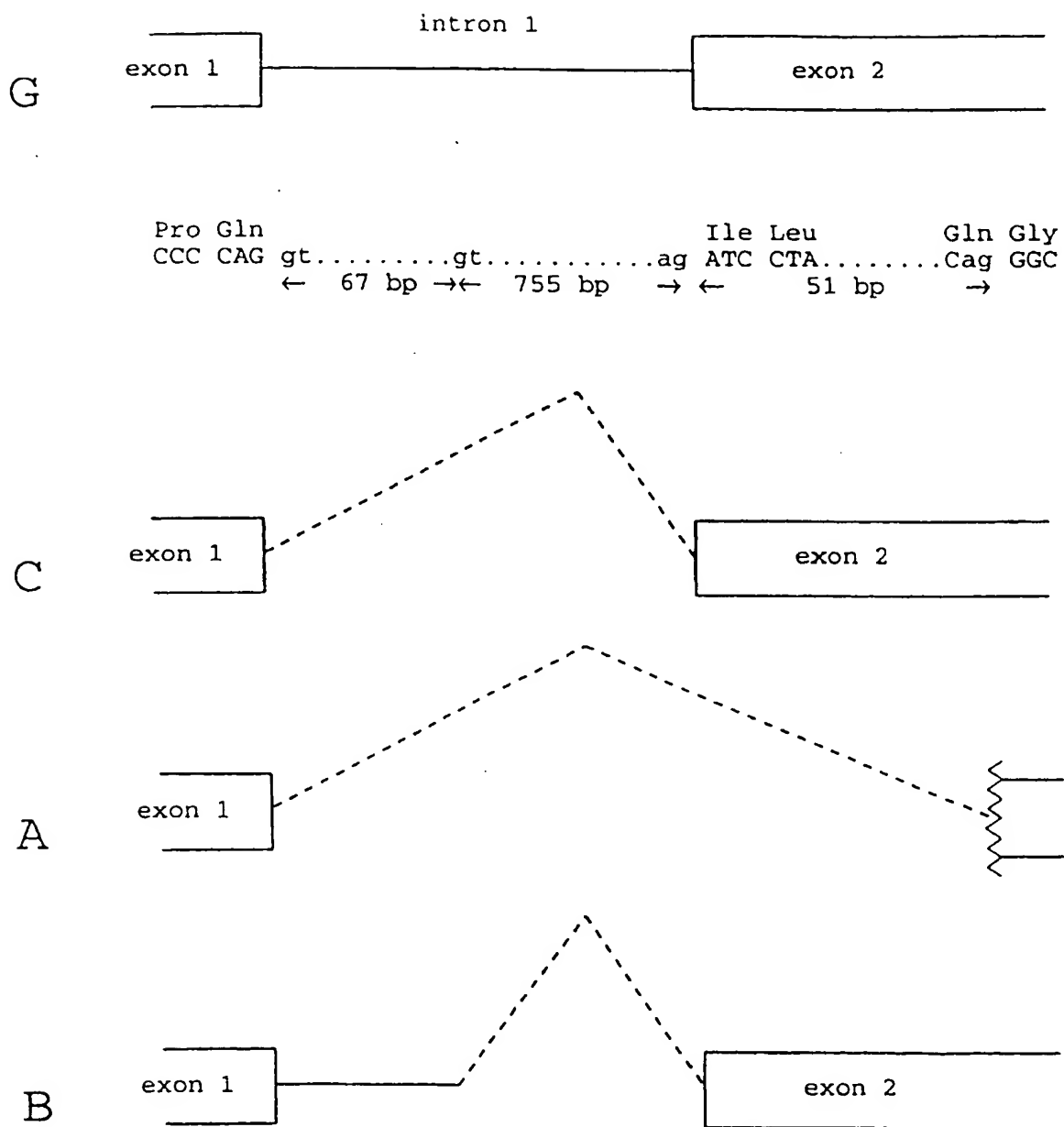


Fig.2C

REPLACEMENT SHEET

13/13

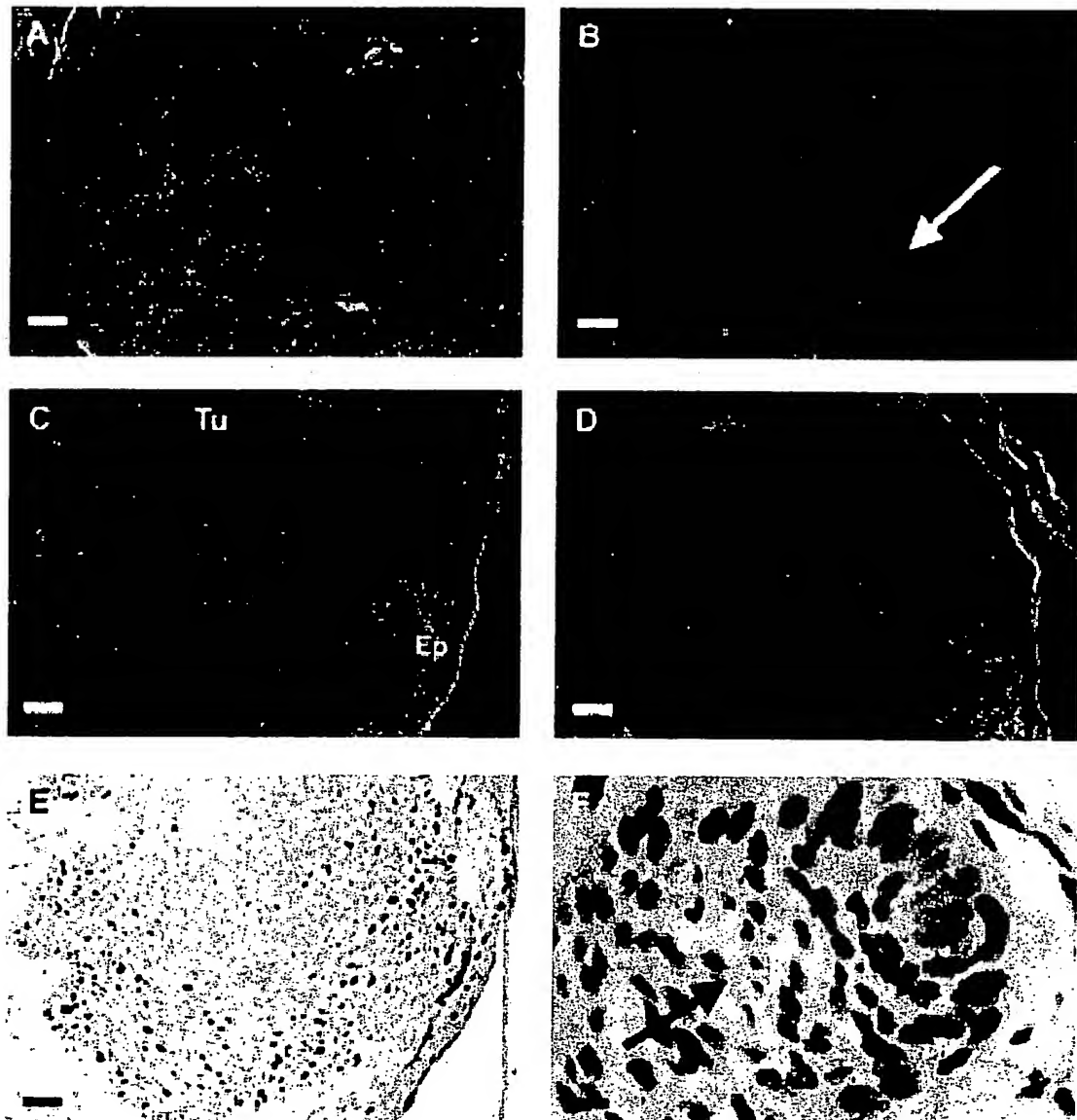


Fig.3

BEST AVAILABLE COPY